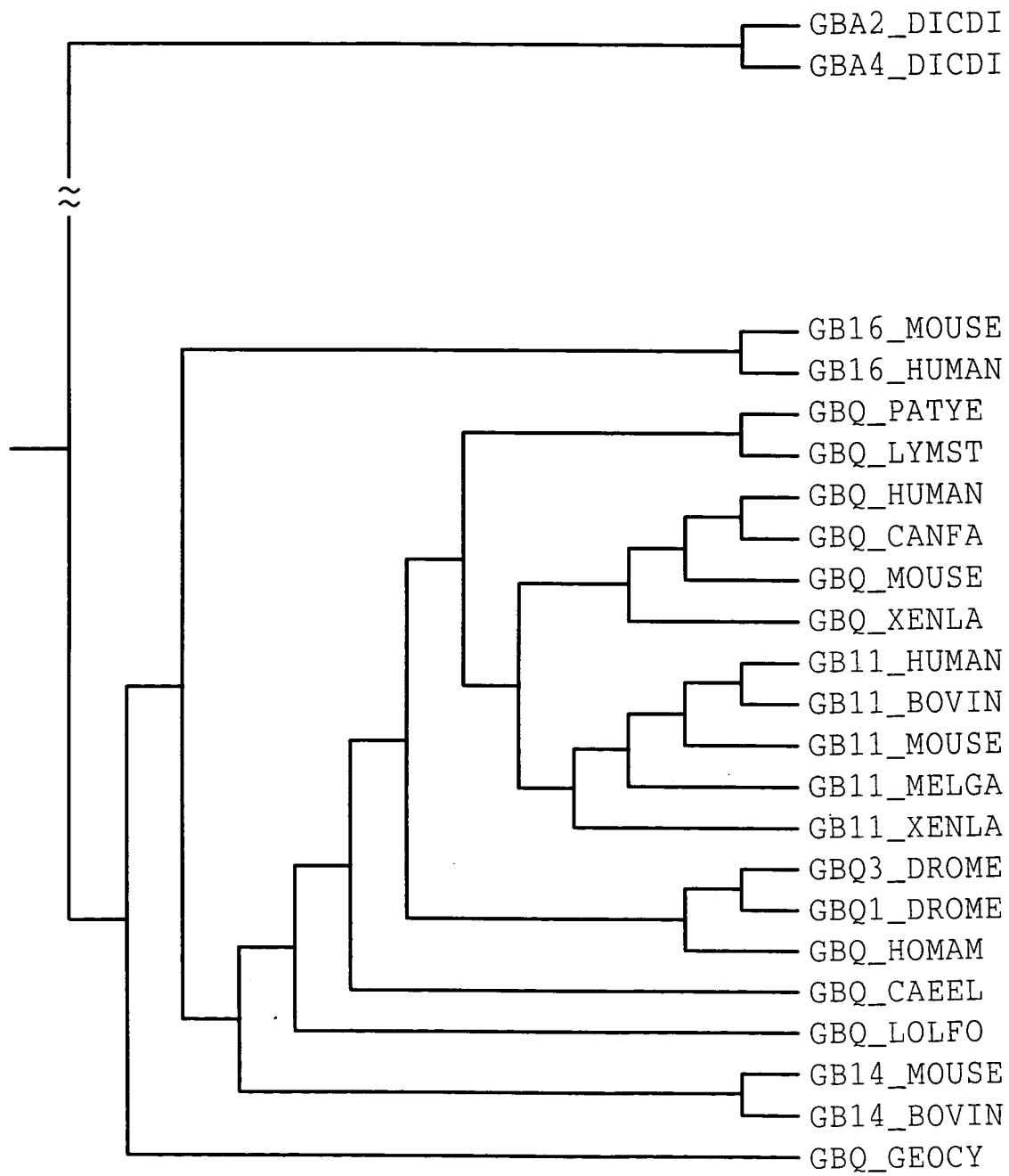


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*C. elegans*  $G\alpha_{q/25}$ 

```

1  MACCLSEEAR  EQKRINQEIE  KQLQORDKRNA  RRELKLLLLG  TGESGKSTFI  KQMRIIHGQG
61 YSEEDKRAHI  RLVYQNVFMA  IQSMIRAMDT  LDIKFGNESE  ELQEKA AVVR  EVDFESVTSF
121 EEPYVSYIKE  LWEDSGIQEC  YDRRREYQLT  DSAKY YLS DL  RRLAVPDYLP  TEQDILRVRV
181 PTTGIIEYPF  DLEQIIIFRMV  DVGGQRSERR  KWIHCFENVT  SIMFLValse  YDQVLVECDN
241 ENRMEESKAL  FRTIITYPWF  TNSSVILFLN  KKD LLEEKIL  YSHLADYFPE  YDGPPRPDPIA
301 AREFILKMFV  DLNPDADKII  YSHFTCATDT  ENIRFVFAAV  KDTILQHNLK  YIGLC

```

*C. elegans*  $G\alpha_{q/29}$ 

```

1  MACCLSEEAR  EQKRINQEIE  KQLQORDKRNA  RRELKLLLLG  TGESGKSTFI  KQMRIIHGQG
61 YSEEDKRAHI  RLVYQNVFMA  IQSMIRAMDT  LDIKFGNESE  ELQEKA AVVR  EVDFESVTSF
121 EEPYVSYIKE  LWEDSGIQEC  YDRRREYQLT  DSAKY YLS DL  RRLAVPDYLP  TEQDILRVRV
181 PTTGIIEYPF  DLEQIIIFRMV  DVGGQRSERR  KWIHCFENVT  SIMFLValse  YDQVLVECDN
241 ENRMEESKAL  FRTIITYPWF  TNSSVILFLN  KKD LLEEKIL  YSHLADYFPE  YDGPPRPDPIA
301 AREFILKMFV  DLNPDADKII  YSHFTCATDT  ENIRFVFAAV  KDTILQNNLK  YIGLC

```

*C. elegans*  $G\alpha_{q/s9}$ 

```

1  MACCLSEEAR  EQKRINQEIE  KQLQORDKRNA  RRELKLLLLG  TGESGKSTFI  KQMRIIHGQG
61 YSEEDKRAHI  RLVYQNVFMA  IQSMIRAMDT  LDIKFGNESE  ELQEKA AVVR  EVDFESVTSF
121 EEPYVSYIKE  LWEDSGIQEC  YDRRREYQLT  DSAKY YLS DL  RRLAVPDYLP  TEQDILRVRV
181 PTTGIIEYPF  DLEQIIIFRMV  DVGGQRSERR  KWIHCFENVT  SIMFLValse  YDQVLVECDN
241 ENRMEESKAL  FRTIITYPWF  TNSSVILFLN  KKD LLEEKIL  YSHLADYFPE  YDGPPRPDPIA
301 AREFILKMFV  DLNPDADKII  YSHFTCATDT  ENIRFVFAAV  KDTILQMHLR  QYELL

```

*C. elegans*  $G\alpha_{q/s21}$ 

```

1  MACCLSEEAR  EQKRINQEIE  KQLQORDKRNA  RRELKLLLLG  TGESGKSTFI  KQMRIIHGQG
61 YSEEDKRAHI  RLVYQNVFMA  IQSMIRAMDT  LDIKFGNESE  ELQEKA AVVR  EVDFESVTSF
121 EEPYVSYIKE  LWEDSGIQEC  YDRRREYQLT  DSAKY YLS DL  RRLAVPDYLP  TEQDILRVRV
181 PTTGIIEYPF  DLEQIIIFRMV  DVGGQRSERR  KWIHCFENVT  SIMFLValse  YDQVLVECDN
241 ENRMEESKAL  FRTIITYPWF  TNSSVILFLN  KKD LLEEKIL  YSHLADYFPE  YDGPPRPDPIA
301 AREFILKMFV  DLNPDADKII  YSHFTCATDT  ENIRRVFND  CD  RDIIQRMHLR  QYELL

```

*C. elegans*  $G\alpha_{q/i3(5)}$ 

```

1  MACCLSEEAR  EQKRINQEIE  KQLQORDKRNA  RRELKLLLLG  TGESGKSTFI  KQMRIIHGQG
61 YSEEDKRAHI  RLVYQNVFMA  IQSMIRAMDT  LDIKFGNESE  ELQEKA AVVR  EVDFESVTSF
121 EEPYVSYIKE  LWEDSGIQEC  YDRRREYQLT  DSAKY YLS DL  RRLAVPDYLP  TEQDILRVRV
181 PTTGIIEYPF  DLEQIIIFRMV  DVGGQRSERR  KWIHCFENVT  SIMFLValse  YDQVLVECDN
241 ENRMEESKAL  FRTIITYPWF  TNSSVILFLN  KKD LLEEKIL  YSHLADYFPE  YDGPPRPDPIA
301 AREFILKMFV  DLNPDADKII  YSHFTCATDT  ENIRFVFAAV  KDTILQHNLK  ECGLY

```

FIGURE 2B

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*D. melanogaster*  $G\alpha_{q/z5}$

1	MECCLSEEA	EQRINQEI	KQLRRDKR	RRELKLLLG	TGESGKSTFI	KQMRIIHGSG
61	YSDDEKRGYI	KLVFQNIFMA	MQSMIKAMDM	LKISYGQGEH	SELADLVMSI	DYETVTTTFED
121	PYLNAIKTLW	DDAGIQECYD	RRREYQLTDS	AKYYLKDLDR	VAQPAYLPTE	QDILRVRVPT
181	TGIIEYPFDL	EEIRFRMVDV	GGQSRERRKW	IHCFENVTSI	IFLVALSEYD	QILFESDNEN
241	RMEESKALFR	TIITYPWFQN	SSVILFLNKK	DLLEEKIMYS	HLVDYFPEYD	GPQRDAITAR
301	EFILRMFVDL	NPDSEKIIYS	HFTCATDTEN	IRFVFAAVKD	TILQSNLKYI	<b>GLC</b>

1. The first step is to identify the problem. This involves understanding the current situation and the goals that need to be achieved.

FIGURE 3

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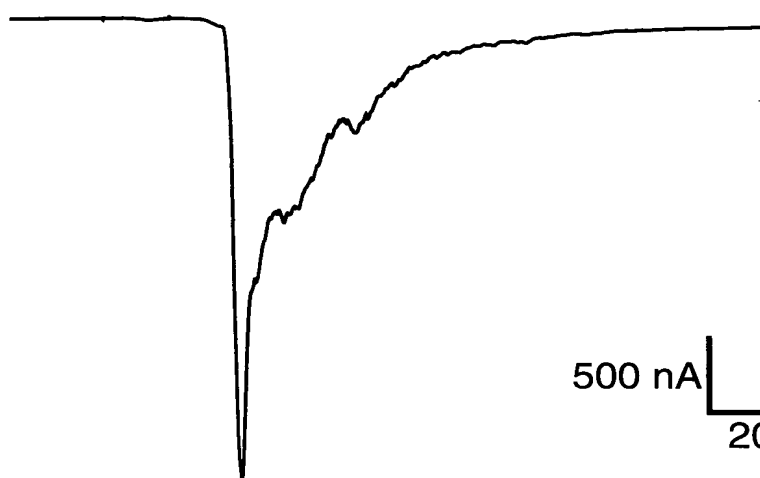
hNPFF1

NPFF 1 $\mu$ M



hNPFF1 + cG $\alpha_{q/z5}$

NPFF 1 $\mu$ M



500 nA  
20 s

hNPFF1 + cG $\alpha_{q/z5}$   
+ 190 ng EGTA

NPFF 1 $\mu$ M



FIGURE 4

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# Human D1

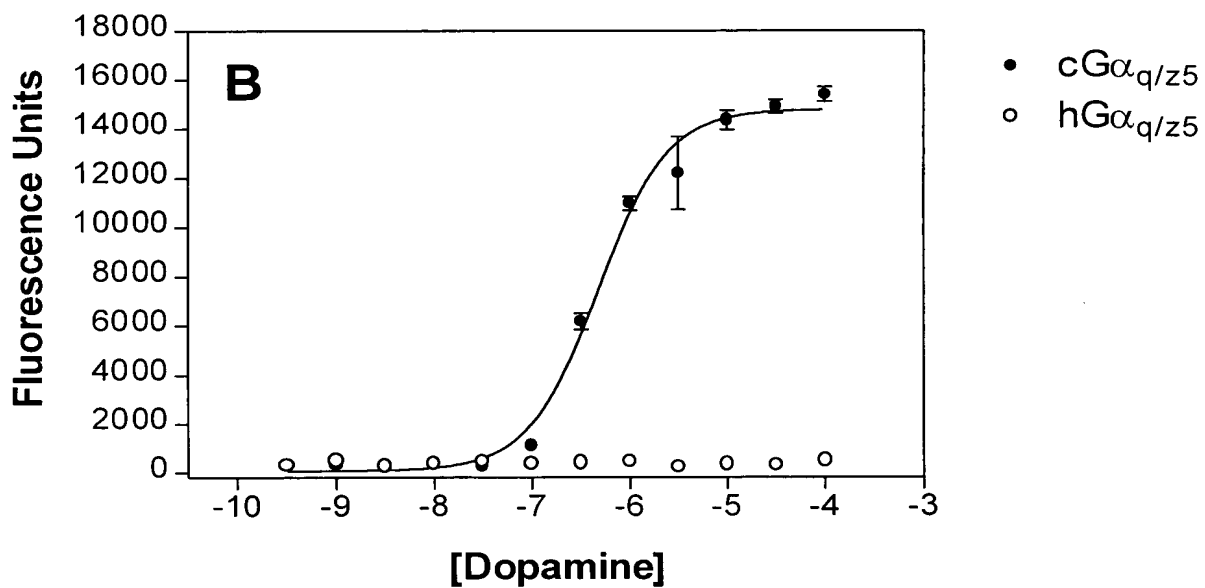
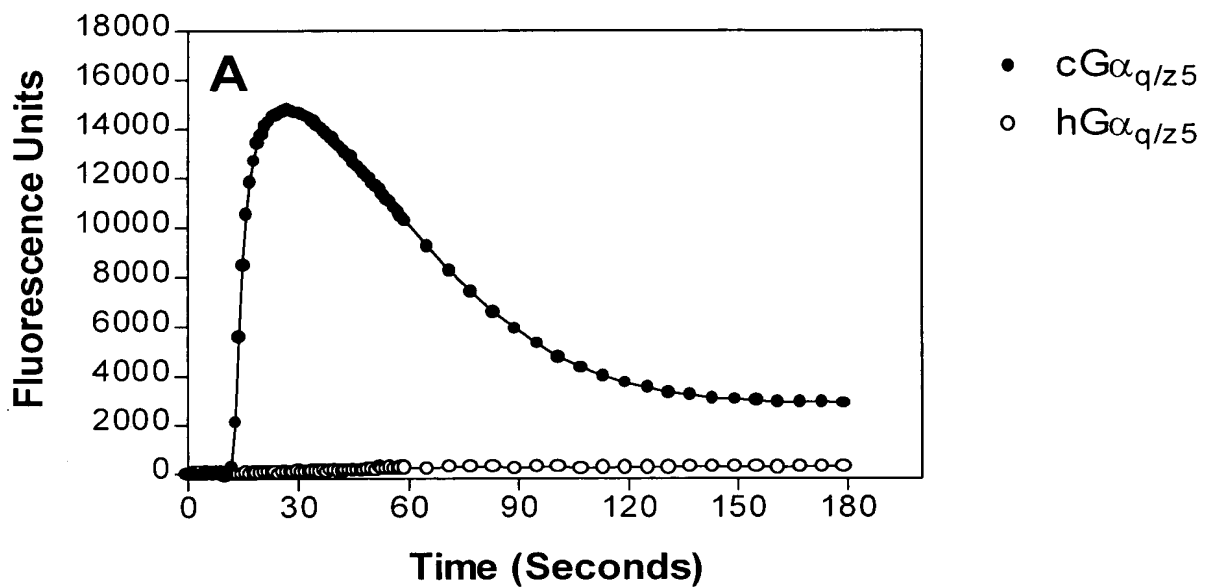


FIGURE 5A

```

      *           20           *           40           *
GBQ_HUMAN : MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARREIKLLLLLGTGES
GBQ_CANFA : MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARREIKLLLLLGTGES
GBQ_MOUSE : MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARREIKLLLLLGTGES
GBQ_XENLA : MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARREIKLLLLLGTGES
GBQ_PATYE : ~~~~~MACCLSEEAKEOKRINCEIEKELRKAKRDARREIKLLLLLGTGES
GBQ_LYMST : ~~~~~MACCIPDELKEOKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ1_DROM : ~~~~~MEGCLSEEAKEOKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ3_DROM : ~~~~~MEGCLSEEAKEOKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ_HOMAM : ~~~~~MACCLSEEAKEOKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ_LIMPO : ~~~~~MACCLSEEGKEOKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ_LOLFO : ~~~~~MACCLSEEAKEOKRINQEIIEKQLRRDKRDARREIKLLLLLGTGES
GBQ_CAEEL : ~~~~~MACCLSEEAKEOKRINQEIIEKQLORDKRNARREIKLLLLLGTGES
GBQ_GEOCY : ~~~~~MSGLLSEERLQKRINTRINRELQRDCHKDAKKEIKLLLLLGTGES

      60           *           80           *           100
GBQ_HUMAN : GKSTFIKQMRIIHGSGYSDEDKRGFTKLVYONIFETAMQAMIRAMDTLKIP
GBQ_CANFA : GKSTFIKQMRIIHGSGYSDEDKRGFTKLVYONIFETAMQAMIRAMDTLKIP
GBQ_MOUSE : GKSTFIKQMRIIHGSGYSDEDKRGFTKLVYONIFETAMQAMIRAMDTLKIP
GBQ_XENLA : GKSTFIKQMRIIHGSGYSDEDKRGFTKLVYONIFETAMQAMIRAMDTLKIP
GBQ_PATYE : GKSTFIKQMRIIHGTGYSEEDKRGFIKIVYONIFEMAMHSMIRAMDTIKIS
GBQ_LYMST : GKSTFIKQMRIIHGAGYSDEDKRSHIKIVYONIFEMAMHAMIRAMDTLNTQ
GBQ1_DROM : GKSTFIKQMRIIHGSGYSDEDKRGYIKLVFONIFEMAMQSMIKAMDMLKIS
GBQ3_DROM : GKSTFIKQMRIIHGSGYSDEDKRGYIKLVFONIFEMAMQSMIKAMDMLKIS
GBQ_HOMAM : GKSTFIKQMRIIHGAGYSDEDKRGFIKLVFONIFEMAMQSMIRAMDLLQIS
GBQ_LIMPO : GKSTFIKQMRIIHGQGYSDDDKKS YIKLVYONIIIMAMQSMNKAMEMKIS
GBQ_LOLFO : GKSTFIKQMRIIHGSGYSEEDKRGFEKIVYONIFESAIQTLTAAMETLSLE
GBQ_CAEEL : GKSTFIKQMRIIHGQGYSEEDKRAHIRLVYONVEMAIQSMIRAMDTLDTK
GBQ_GEOCY : GKSTFIKQMRIIHGKGYSKQDLCLEYKNLMFRNIIILMSMHSMLQATAELKIA

      *           120           *           140           *
GBQ_HUMAN : YKYEHNK--AHAQLVREVDVEKVS----AFENPYVDAIKSLWNDPGIQEC
GBQ_CANFA : YKYEHNK--AHAQLVREVDVEKVS----AFENPYVDAIKSLWNDPGIQEC
GBQ_MOUSE : YKYEHNK--AHAQLVREVDVEKVS----AFENPYVDAIKSLWNDPGIQEC
GBQ_XENLA : YKYEHNK--GHALLVREVDVEKVA----SFENPYVDAIKYLWNDPGIQEC
GBQ_PATYE : FEVADNE--ENAIMIROVDYETVT----TLDSQSVEATLSLWADAGIQEC
GBQ_LYMST : YINPANR--ENGNMIRQIDYETVT----TEDKPCVDATISLWNDGDIQEC
GBQ1_DROM : YGQGEHS--ELADLVMSIDYETVT----TEDPYLNAIKTLWDDAGIQEC
GBQ3_DROM : YGQGEHS--ELADLVMSIDYETVT----TEDPYLNAIKTLWDDAGIQEC
GBQ_HOMAM : YGDSANI--EHADLVRSVDYESVT----TEEPYVTAMNSLWQDTGTQHHC
GBQ_LIMPO : YKDRNNI--ENAEVLVSVDYETVT----TEDSPYVEATIKSLWVDPGIQEC
GBQ_LOLFO : YKDPSN--NEHAFLNSIDADSAD----IEEDGHVTAIKGCWTDPGMQEC
GBQ_CAEEL : FGNESEELQEKAAVVREVDVESVT----SEEPYVSYIKELWEDSGIQEC
GBQ_GEOCY : YIDPD--AQRHVQLLMALRPETAQ----SLGGETCEATIRKLWQDAGVQEC

```

FIGURE 5B

GBQ\_HUMAN : YDRRREYQ - LSDSTKYYLNDLDRVADPAYLEPTQQDVLRRVRVPTTGITIEYP  
 GBQ\_CANFA : YDRRREYQ - LSDSTKYYLNDLDRVADPAYLEPTQQDVLRRVRVPTTGITIEYP  
 GBQ\_MOUSE : YDRRREYQ - LSDSTKYYLNDLDRVADPSYLEPTQQDVLRRVRVPTTGITIEYP  
 GBQ\_XENLA : YDRRREYQ - LSDSTKYYLNDLDRIATHGYLEPTQQDVLRRVRVPTTGITIEYP  
 GBQ\_PATYE : YDRRREYQ - LTDSAKYYLDAVDRIAEFNYLEPTLODILRRVRVPTTGITIEYP  
 GBQ\_LYMST : YDRRREYQ - LTDSAKYYLDSVERISQQDYLEPTLODILRRVRVPTTGITIEYP  
 GBQ1\_DROM : YDRRREYQ - LTDSAKYYLSDLARIEQADYLEPTEQDILRRVRVPTTGITIEYP  
 GBQ3\_DROM : YDRRREYQ - LTDSAKYYLKDLDRAVQPAYLEPTEQDILRRVRVPTTGITIEYP  
 GBQ\_HOMAM : YDRRREYQ - LTDSAKYYLTDLRIAADKYVSTLODILRRVRVPTTGITIEYP  
 GBQ\_LIMPO : YDRRREYQ - LTDSAKYYLNDIDRIAVPNYLEPTQDILRRVRVPTTGITIEYP  
 GBQ\_LOLFO : YDRRREYQ - LTDSAKYYLDDVERIHEPGYIPTLODILRRVRVPTTGITIEYP  
 GBQ\_CAEEL : YDRRREYQ - LTDSAKYYLSDLRRLAVPDYLEPTEQDILRRVRVPTTGITIEYP  
 GBQ\_GEOCY : YDRRREYQ - LSDSTKYYLDDLPRISSNDYVPTTQDVLRRVRVPTTGITIEYP

GBQ\_HUMAN : FDLQSVIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_CANFA : FDLQSVIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_MOUSE : FDLQSVIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_XENLA : FDLQSVIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_PATYE : FDLDSIIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_LYMST : FDLDSIIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ1\_DROM : FDLDGIVIFRMVDVGGQSRERRKWIHCFENVTSIIFLVALSEYDOILFESD  
 GBQ3\_DROM : FDLLEEIRFRMVDVGGQSRERRKWIHCFENVTSIIFLVALSEYDOILFESD  
 GBQ\_HOMAM : FDLLEEIRFRMVDVGGQSRERRKWIHCFENVTSIIFLVALSEYDOILFESD  
 GBQ\_LIMPO : FILDSSIIFRMVDVGGQSRERRKWIHCFENVTSIIFLVALSEYDOILFESD  
 GBQ\_LOLFO : FDLYSIIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_CAEEL : FDLQSVIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOVLVESD  
 GBQ\_GEOCY : FTINKIIFRMVDVGGQSRERRKWIHCFENVTSIMFLVALSEYDOILVESD

GBQ\_HUMAN : N-ENRMEESKALFRTITITYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_CANFA : N-ENRMEESKALFRTITITYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_MOUSE : N-ENRMEESKALFRTITITYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_XENLA : N-ENRMEESKALFRTITITYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_PATYE : N-ENRMEESKALFRTITITYPWFONSSVILFLNKKDLLEEKIMHSHLVDYF  
 GBQ\_LYMST : N-ENRMEESKALFRTITITYPWFONSSVILFLNKKDLLEEKIMHSHLVDYF  
 GBQ1\_DROM : N-ENRMEESKALFRTITITYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ3\_DROM : N-ENRMEESKALFRTITITYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_HOMAM : N-ENRMEESKALFKTITITYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_LIMPO : N-ENRMEESKALFKTITITYPWFONSSVILFLNKKDLLEEKIMFSHLVDYF  
 GBQ\_LOLFO : N-ENRMEESKALFRTITITYPWFONSSVILFLNKKDLLEEKIMTSHLVDYF  
 GBQ\_CAEEL : N-ENRMEESKALFRTITITYPWFONSSVILFLNKKDLLEEKIMYSHLVDYF  
 GBQ\_GEOCY : SRVNRMVESLHLFNTITISYFENKSSIILFLNKKDLLEEKIMHSHLVDYF

FIGURE 5C

GBQ\_HUMAN : PEYDGPQRDAQAAREFLLKMFVDLNPDSDKITLYSHETCATDTENIRFVFA  
 GBQ\_CANFA : PEYDGPQRDAQAAREFLLKMFVDLNPDSDKITLYSHETCATDTENIRFVFA  
 GBQ\_MOUSE : PEYDGPQRDAQAAREFLLKMFVDLNPDSDKITLYSHETCATDTENIRFVFA  
 GBQ\_XENLA : PEYDGPQRDAQAAREFLLKMFVDLNPDSDKITLYSHETCATDTENIRFVFA  
 GBQ\_PATYE : PEFDGQKKDAQCAREFTLRMEVDLNPDPDKITLYSHETCATDTENIRFVFA  
 GBQ\_LYMST : PEFDGPKKEASTAREFTLRMEVELNPDPDKITLYSHETCATDTENIRFVFA  
 GBQ1\_DROM : PEYDGPQKQDHAAAKQFVKKYLACNPDPERQCYSHETTATDTENIKLVFC  
 GBQ3\_DROM : PEYDGPQRDAITAREFTLRMEVDLNPDSKITYSHETCATDTENIRFVFA  
 GBQ\_HOMAM : PEYDGPQRDAITAAREFTLRMEVELNPDPKITYSHETCATDTENIRFVFA  
 GBQ\_LIMPO : PEYDGPKKDAVOGREFLLKMFVDLNPDSKITYSHETCATDTENIRFVFA  
 GBQ\_LOLFO : PDYDGPKCDYEAAREFMMSYMDLNECKEKMLYYHYTCATDTENIRFVFA  
 GBQ\_CAEEL : PEYDGPPRDPIAAREFTLRMEVDLNPADKITYSHETCATDTENIRFVFA  
 GBQ\_GEOCY : EYDGPKCDHVSARESLAKMESISINDMRSADITYPHETCATDTENIKEVFD

GBQ\_HUMAN : AVKDTIILQLNLKEYNAV~~~ : 359  
 GBQ\_CANFA : AVKDTIILQLNLKEYNLV~~~ : 359  
 GBQ\_MOUSE : AVKDTIILQLNLKEYNLV~~~ : 359  
 GBQ\_XENLA : AVKDTIILQLNLKEYNLV~~~ : 359  
 GBQ\_PATYE : AVKDTIILQLNLKEYNLV~~~ : 353  
 GBQ\_LYMST : AVKDTIILQLNLKEYNLV~~~ : 353  
 GBQ1\_DROM : AVKDTIMONALKEFNLC~~~ : 353  
 GBQ3\_DROM : AVKDTIILQSNLKEYNLV~~~ : 353  
 GBQ\_HOMAM : AVKDTIILQLNLKEYNLV~~~ : 353  
 GBQ\_LIMPO : AVKDTIILQLNLKEYNLV~~~ : 353  
 GBQ\_LOLFO : AVKDTIILQLNLKEYNLV~~~ : 354  
 GBQ\_CAEEL : AVKDTIILQHNLEKEYNLV~~~ : 355  
 GBQ\_GEOCY : VVKNHILQQHITE--VVPGL : 355